

My experiment with open science: taking the benefits of sharing beyond source code

Carl Boettiger

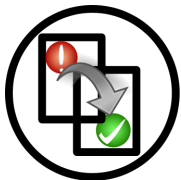
UC Davis

June 30, 2010

Why Open Source?



**Reproduce
Research**



Find & Fix Bugs



**Extend: New
Software**



Share



Link Data



Link People

Code



Literature



Discussions



Lab Notebook





Share

Open Source Licenses





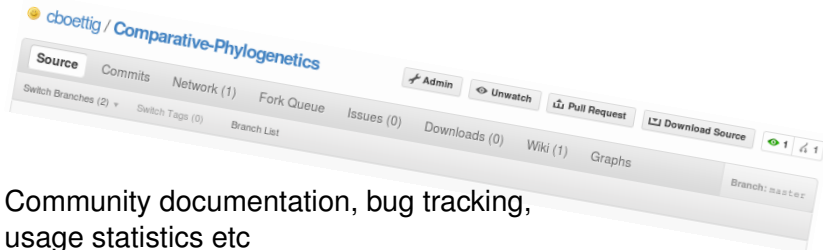
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Version Manage



```
R/data2ouch.R
... @8 -6,12 +6,13 @8
6
7 data2ouch <- function(tree, data){
8   ot <- ape2ouch(tree)
9   + data <- as.data.frame(data)
10  # otd <- as(ot, "data.frame")
11  otd <- data.frame(nodes = as.integer(ot@nodes), ancestors = ot@ancestors, times = ot@times, labels = ot@odelabels)
12  data$labels <- rownames(data)
13  otd <- merge(otd, data, by="labels", all=T)
14  - rownames(otd) = otd$nodes
15  + otd$ancestors <- as.integer(ot@ancestors)
```

Search

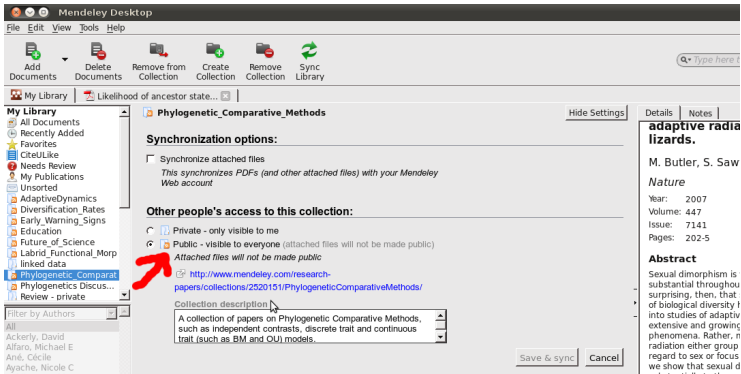


Community documentation, bug tracking,
usage statistics etc





Share



The screenshot shows the Mendeley Desktop application window. The title bar reads "Mendeley Desktop". The menu bar includes "File", "Edit", "View", "Tools", and "Help". The toolbar contains icons for "Add Documents", "Delete Documents", "Remove from Collection", "Create Collection", "Remove Collection", and "Sync Library". Below the toolbar, there are tabs for "My Library" and "Likelihood of ancestor state...".

The "My Library" sidebar on the left lists various collections, including "All Documents", "Recently Added", "Favorites", "CiteULike", "Needs Review", "My Publications", "Unsorted", "AdaptiveDynamics", "Diversification_Rates", "Early_Warning_Signs", "Education", "Future_of_Science", "Labrid_Functional_Morp", "linked data", "Phylogenetic_Comparat...", "Phylogenetics Discus...", and "Review - private". The "Phylogenetic_Comparat..." collection is selected.

The main pane displays the settings for the "Phylogenetic_Comparative_Methods" collection. It includes a "Synchronization options:" section with a checkbox for "Synchronize attached files" and a description: "This synchronizes PDFs (and other attached files) with your Mendeley Web account". Below this is the "Other people's access to this collection:" section, which has two radio button options: "Private - only visible to me" and "Public - visible to everyone (attached files will not be made public)". The "Public" option is selected. A red arrow points to the "Public" option. Below the radio buttons, there is a link to the collection's URL: <http://www.mendeley.com/research-papers/collections/2520151/PhylogeneticComparativeMethods/>. A "Collection description" box is also visible, containing the text: "A collection of papers on Phylogenetic Comparative Methods, such as independent contrasts, discrete trait and continuous trait (such as BM and OUI models).". At the bottom right of the main pane are "Save & sync" and "Cancel" buttons.

On the right side of the window, there are tabs for "Details" and "Notes". The "Details" tab is active, showing information about the collection, including the title "adaptive radiations in lizards.", the author "M. Butler, S. Saw", the year "2007", the volume "447", the issue "7141", and the pages "202-5". The "Abstract" section is also visible, starting with "Sexual dimorphism is substantial throughout surprising, then, that of biological diversity I into studies of adaptive extensive and growing phenomena. Rather, n radiation either group regard to sex or focus we show that sexual d".



Link Data

Browse Papers ▼

Browse Collections

Search research papers

Search for papers

GENETICS (BIOLOGICAL SCIENCES)

Toward extracting all phylogenetic information from matrices of evolutionary distances.

Sebastien Roch

Like

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Science New York NY (2010)

Volume: 327, Issue: 5971, Pages: 1376-9

ISSN: 10959203

DOI: 10.1126/science.1182300, PubMed ID: 20223986

Available from www.ncbi.nlm.nih.gov

Abstract

The matrix of evolutionary distances is a model-based statistic, derived from molecular sequences, summarizing the pairwise phylogenetic relations between a collection of species. Phylogenetic tree reconstruction methods relying on this matrix are relatively fast and thus widely used in molecular systematics. However, because of their intrinsic reliance on summary statistics, distance-matrix methods are assumed to be less accurate than likelihood-based approaches. In this paper, pairwise sequence comparisons are shown to be more powerful than previously hypothesized. A statistical analysis of certain distance-based techniques indicates that their data requirement for large evolutionary trees essentially matches the conjectured performance of maximum likelihood methods—challenging the idea that summary statistics lead to suboptimal analyses. On the basis of a connection between ancestral state reconstruction and distance measures, the effect is explained by the

Readership Statistics

15 Readers on Mendeley

by Discipline

73% Biological Sciences

7% Computer and Information Science

7% Medicine

by Academic Status

40% Ph.D. Student

27% Post Doc

13% Researcher (at an Academic Institution)

by Country

20% United Kingdom

20% United States

13% Canada

Related Research

Phylogenetic Inference with Weighted Codon



Link People



Carl Boettiger in the Shared Collection **Phylogenetics Discussion Group**



Added "**Tempo and mode of evolutionary radiation in iguanian lizards.**"

15th April - [comment](#) - [like](#)



Carl Boettiger in the Shared Collection **Methods Papers**



Added "**Morphogen Gradients: Limits to Signaling or Limits to Measurement?**"

18th March - [comment](#) - [like](#)



Methods Papers



Jacques Bothma and **Carl Boettiger** have joined your Shared Collection

18th March - [comment](#) - [like](#)



Alistair Boettiger in the Shared Collection **Methods Papers**



Added "**Sub-diffraction-limit imaging by stochastic optical reconstruction microscopy (STORM)**"



Added "**Super-resolution microscopy by nanoscale localization of photo-switchable fluorescent probes.**"



Added "**Three-Dimensional Super-Resolution Imaging by Stochastic Optical Reconstruction Microscopy Supporting online Material**"

Discussion



Share



How do I find the distance between two nodes in a binary tree? Equivalently, what algorithms are there for finding the most recent common ancestor (lowest common ancestor) of two nodes?

algorithm

binary-trees



Link Data

tagged

algorithm × 5480

binary-trees × 224

asked

5 months ago

viewed

574 times

latest activity

5 months ago



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edited Jan 25 at 18:59



Bart K.

12.7k ● 1 ● 13 ● 26

asked Jan 25 at 18:29




Carl

95 ● 4



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User:Carl Boettiger/Notebook/Comparative Phylogenetics

< User:Carl Boettiger | Notebook

<< June 2010 >>

| S | M | T | W | T | F | S |
|----|----|----|----|----|----|----|
| 30 | 31 | 1 | 2 | 3 | 4 | 5 |
| 6 | 7 | 8 | 9 | 10 | 11 | 12 |
| 13 | 14 | 15 | 16 | 17 | 18 | 19 |
| 20 | 21 | 22 | 23 | 24 | 25 | 26 |
| 27 | 28 | 29 | 30 | 1 | 2 | 3 |
| 4 | 5 | 6 | 7 | 8 | 9 | 10 |



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New Approaches for Comparative Phylogenetics with Continuous Traits

Abstract

Phylogenetically based comparative methods are an established and rapidly expanding area of research in macroevolution. Existing approaches may produce misleading results when the traits under consideration reflect different



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System Size Expansion

- Analytic calculation captures the noise propagation through the age structure correctly. This can lead to much larger estimates of the impact of demographic stochastically than previously believed.
- This covariance mechanism requires coupling through the nonlinear terms, otherwise it can simply cancel out. The asymmetric, nonlinear term such as in the generalized crowley model seems to be the simplest way to produce a large demographic noise effect:

$$\partial_i f_i \ll \partial_i f_j$$

- Earlier descriptions have failed to include the connections in the noise structure, i.e. from [Dennis et al 2001](#) "that the noise variables are uncorrelated with each other within a time unit (off-diagonal elements of the matrix are zero)."
- Two interesting side-questions have emerged -- the influence of the two-step vs one-step transitions and the connections of multiple stages. [\[edit\]](#)

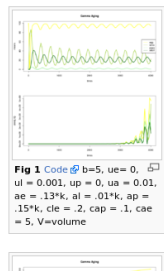


Fig 1. Code [b=5, ue= 0, ul = 0.001, up = 0, ua = 0.01, ae = .13*k, al = .01*k, ap = .15*k, cle = .2, cap = .1, cae = 5, V=volume](#)



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changes
contributions

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ages
version
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Mietten ▾

Contact Info

[edit]

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- University of Jena [✉](#)
- Structural Brain Mapping Group [✉](#)
- Jahnstr. 3, 07743 Jena, Germany [✉](#)
- Email me through OpenWetWare
- Other online coordinates: Blog [✉](#) Citizendium [✉](#) Friendfeed [✉](#) Band [✉](#), Google [✉](#)

Education


[edit]

- 2006, PhD (Physics), University of the Saarland [✉](#) & Fraunhofer Institute for Biomedical Engineering [✉](#)
3D Magnetic Resonance Microscopy of Dehydrated Biological Specimens (pdf [B](#))
- 2001, MS (Biophysics), Humboldt University [✉](#)
The temperature dependence of electrorotation - automated dielectric single-cell spectroscopy (pdf [B](#))
- 1998, BS (Biophysics/Biochemistry), Institut Jacques Monod [✉](#) & University of Paris VII [✉](#) & Humboldt University [✉](#)
Catalytic activities of alternative hammerhead ribozymes

Research interests

[edit]

1. Brain morphometry [✉](#)
2. Non-invasive imaging



[edit]

Conclusions

- Faster, Better, Broader Impact
- Exponentially growing science: need solutions that scale
- Building networks, building community

